

## SEQUENCE LISTING

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<110> Caput, Daniel  
Ferrara, Pascual  
Kaghad, Ahmed Mourad  
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FEB 01 2000

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CCG CCA CCC CCA GGC ACT GCC ATC CGG GCC ATG CCT GTT TAC AAG AAA Pro Pro Pro Pro Gly Thr Ala Ile Arg Ala Met Pro Val Tyr Lys Lys 170 175 180	581
GCG GAG CAC GTG ACC GAC GTC GTG AAA CGC TGC CCC AAC CAC GAG CTC Ala Glu His Val Thr Asp Val Val Lys Arg Cys Pro Asn His Glu Leu 185 190 195	629
GGG AGG GAC TTC AAC GAA GGA CAG TCT GCT CCA GCC AGC CAC CTC ATC Gly Arg Asp Phe Asn Glu Gly Gln Ser Ala Pro Ala Ser His Leu Ile	677

200	205	13 210	215	
CGC GTG GAA GGC AAT AAT CTC TCG CAG TAT GTG GAT GAC CCT GTC ACC Arg Val Glu Gly Asn Asn Leu Ser Gln Tyr Val Asp Asp Pro Val Thr 220 225 230				725
GGC AGG CAG AGC GTC GTG CCC TAT GAG CCA CCA CAG GTG GGG ACG Gly Arg Gln Ser Val Val Val Pro Tyr Glu Pro Pro Gln Val Gly Thr 235 240 245				773
GAA TTC ACC ACC ATC CTG TAC AAC TTC ATG TGT AAC AGC AGC TGT GTA Glu Phe Thr Thr Ile Leu Tyr Asn Phe Met Cys Asn Ser Ser Cys Val 250 255 260				821
GGG GGC ATG AAC CGG CGG CCC ATC CTC ATC ATC ACC CTG GAG ATG Gly Gly Met Asn Arg Arg Pro Ile Leu Ile Ile Thr Leu Glu Met 265 270 275				869
CGG GAT GGG CAG GTG CTG GGC CGC CGG TCC TTT GAG GGC CGC ATC TGC Arg Asp Gly Gln Val Leu Gly Arg Arg Ser Phe Glu Gly Arg Ile Cys 280 285 290 295				917
GCC TGT CCT GGC CGC GAC CGA AAA GCT GAT GAG GAC CAC TAC CGG GAG Ala Cys Pro Gly Arg Asp Arg Lys Ala Asp Glu Asp His Tyr Arg Glu 300 305 310				965
CAG CAG GCC CTG AAC GAG AGC TCC GCC AAG AAC GGG GCC GCC AGC AAG Gln Gln Ala Leu Asn Glu Ser Ser Ala Lys Asn Gly Ala Ala Ser Lys 315 320 325				1013
CGT GCC TTC AAG CAG AGC CCC CCT GCC GTC CCC GCC CTT GGT GCC GGT Arg Ala Phe Lys Gln Ser Pro Pro Ala Val Pro Ala Leu Gly Ala Gly 330 335 340				1061
<i>AS</i> GTG AAG AAG CGG CGG CAT GGA GAC GAG GAC ACG TAC TAC CTT CAG GTG Val Lys Lys Arg Arg His Gly Asp Glu Asp Thr Tyr Tyr Leu Gln Val 345 350 355				1109
CGA GGC CGG GAG AAC TTT GAG ATC CTG ATG AAG CTG AAA GAG AGC CTG Arg Gly Arg Glu Asn Phe Glu Ile Leu Met Lys Leu Lys Glu Ser Leu 360 365 370 375				1157
GAG CTG ATG GAG TTG GTG CCG CAG CCA CTG GTG GAC TCC TAT CGG CAG Glu Leu Met Glu Leu Val Pro Gln Pro Leu Val Asp Ser Tyr Arg Gln 380 385 390				1205
CAG CAG CAG CTC CTA CAG AGG CCG AGT CAC CTA CAG CCC CCG TCC TAC Gln Gln Gln Leu Leu Gln Arg Pro Ser His Leu Gln Pro Pro Ser Tyr 395 400 405				1253
GGG CCG GTC CTC TCG CCC ATG AAC AAG GTG CAC GGG GGC ATG AAC AAG Gly Pro Val Leu Ser Pro Met Asn Lys Val His Gly Gly Met Asn Lys 410 415 420				1301
CTG CCC TCC GTC AAC CAG CTG GTG GGC CAG CCT CCC CCG CAC AGT TCG Leu Pro Ser Val Asn Gln Leu Val Gly Gln Pro Pro Pro His Ser Ser 425 430 435				1349

GCA GCT ACA CCC AAC CTG GGG CCC GTG GGC CCC GGG ATG CTC AAC AAC Ala Ala Thr Pro Asn Leu Gly Pro Val Gly Pro Gly Met Leu Asn Asn 440 445 450 455	1397
CAT GGC CAC GCA GTG CCA GCC AAC GGC GAG ATG AGC AGC AGC CAC AGC His Gly His Ala Val Pro Ala Asn Gly Glu Met Ser Ser Ser His Ser 460 465 470	1445
GCC CAG TCC ATG GTC TCG GGG TCC CAC TGC ACT CCG CCA CCC CCC TAC Ala Gln Ser Met Val Ser Gly Ser His Cys Thr Pro Pro Pro Pro Tyr 475 480 485	1493
CAC GCC GAC CCC AGC CTC GTC AGT TTT TTA ACA GGA TTG GGG TGT CCA His Ala Asp Pro Ser Leu Val Ser Phe Leu Thr Gly Leu Gly Cys Pro 490 495 500	1541
AAC TGC ATC GAG TAT TTC ACC TCC CAA GGG TTA CAG AGC ATT TAC CAC Asn Cys Ile Glu Tyr Phe Thr Ser Gln Gly Leu Gln Ser Ile Tyr His 505 510 515	1589
CTG CAG AAC CTG ACC ATT GAG GAC CTG GGG GCC CTG AAG ATC CCC GAG Leu Gln Asn Leu Thr Ile Glu Asp Leu Gly Ala Leu Lys Ile Pro Glu 520 525 530 535	1637
CAG TAC CGC ATG ACC ATC TGG CGG GGC CTG CAG GAC CTG AAG CAG GGC Gln Tyr Arg Met Thr Ile Trp Arg Gly Leu Gln Asp Leu Lys Gln Gly 540 545 550	1685
CAC GAC TAC AGC ACC GCG CAG CAG CTG CTC CGC TCT AGC AAC GCG GCC His Asp Tyr Ser Thr Ala Gln Gln Leu Leu Arg Ser Ser Asn Ala Ala 555 560 565	1733
AS ✓ACC ATC TCC ATC GGC GGC TCA GGG GAA CTG CAG CGC CAG CGG GTC ATG Thr Ile Ser Ile Gly Gly Ser Gly Glu Leu Gln Arg Gln Arg Val Met 570 575 580	1781
GAG GCC GTG CAC TTC CGC GTG CGC CAC ACC ATC ACC CCC AAC CGC Glu Ala Val His Phe Arg Val Arg His Thr Ile Thr Ile Pro Asn Arg 585 590 595	1829
GGC GGC CCA GGC GGC CCT GAC GAG TGG GCG GAC TTC GGC TTC GAC Gly Gly Pro Gly Gly Pro Asp Glu Trp Ala Asp Phe Gly Phe Asp 600 605 610 615	1877
CTG CCC GAC TGC AAG GCC CGC AAG CAG CCC ATC AAG GAG GAG TTC ACG Leu Pro Asp Cys Lys Ala Arg Lys Gln Pro Ile Lys Glu Glu Phe Thr 620 625 630	1925
GAG GCC GAG ATC CAC TGAGGGCCTC GCCTGGCTGC AGCCTGCGCC ACCGCCAGA Glu Ala Glu Ile His 635	1980
GACCCAAGCT GCCTCCCCCTC TCCTTCCTGT GTGTCCAAAA CTGCCTCAGG AGGCAGGACC	2040
TTCGGGCTGT GCCCGGGGAA AGGCAAGGTC CGGCCCATCC CCAGGCACCT CACAGGCC	2100

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20															25

Gln	Ser	Ser	Arg	Gly	Asn	Asn	Glu	Val	Val	Gly	Gly	Thr	Asp	Ser	Ser
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35															40

Met	Asp	Val	Phe	His	Leu	Glu	Gly	Met	Thr	Thr	Ser	Val	Met	Ala	Gln
															60
50															55

Phe	Asn	Leu	Leu	Ser	Ser	Thr	Met	Asp	Gln	Met	Ser	Ser	Arg	Ala	Ala
															80
65															70

Ser	Ala	Ser	Pro	Tyr	Thr	Pro	Glu	His	Ala	Ala	Ser	Val	Pro	Thr	His
															95
85															90

Ser	Pro	Tyr	Ala	Gln	Pro	Ser	Ser	Thr	Phe	Asp	Thr	Met	Ser	Pro	Ala
															110
100															105

Pro	Val	Ile	Pro	Ser	Asn	Thr	Asp	Tyr	Pro	Gly	Pro	His	His	Phe	Glu
															125
115															120

Val	Thr	Phe	Gln	Gln	Ser	Ser	Thr	Ala	Lys	Ser	Ala	Thr	Trp	Thr	Tyr
															140
130															135

Ser	Pro	Leu	Leu	Lys	Lys	Leu	Tyr	Cys	Gln	Ile	Ala	Lys	Thr	Cys	Pro
															160
145															150

Ile	Gln	Ile	Lys	Val	Ser	Thr	Pro	Pro	Pro	Gly	Thr	Ala	Ile	Arg	
															175
165															170

Ala	Met	Pro	Val	Tyr	Lys	Lys	Ala	Glu	His	Val	Thr	Asp	Val	Val	Lys
															190
180															185

Arg	Cys	Pro	Asn	His	Glu	Leu	Gly	Arg	Asp	Phe	Asn	Glu	Gly	Gln	Ser
															205
195															200

Ala	Pro	Ala	Ser	His	Leu	Ile	Arg	Val	Glu	Gly	Asn	Asn	Leu	Ser	Gln
															220
210															215

Tyr	Val	Asp	Asp	Pro	Val	Thr	Gly	Arg	Gln	Ser	Val	Val	Val	Pro	Tyr
															240
225															230

Glu	Pro	Pro	Gln	Val	Gly	Thr	Glu	Phe	Thr	Thr	Ile	Leu	Tyr	Asn	Phe
															255
245															250

*ASW*

Met Cys Asn Ser Ser Cys Val Gly Gly Met Asn Arg Arg Pro Ile Leu  
 260 265 270

Ile Ile Ile Thr Leu Glu Met Arg Asp Gly Gln Val Leu Gly Arg Arg  
 275 280 285

Ser Phe Glu Gly Arg Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala  
 290 295 300

Asp Glu Asp His Tyr Arg Glu Gln Gln Ala Leu Asn Glu Ser Ser Ala  
 305 310 315 320

Lys Asn Gly Ala Ala Ser Lys Arg Ala Phe Lys Gln Ser Pro Pro Ala  
 325 330 335

Val Pro Ala Leu Gly Ala Gly Val Lys Lys Arg Arg His Gly Asp Glu  
 340 345 350

Asp Thr Tyr Tyr Leu Gln Val Arg Gly Arg Glu Asn Phe Glu Ile Leu  
 355 360 365

Met Lys Leu Lys Glu Ser Leu Glu Leu Met Glu Leu Val Pro Gln Pro  
 370 375 380

Leu Val Asp Ser Tyr Arg Gln Gln Gln Leu Leu Gln Arg Pro Ser  
 385 390 395 400

His Leu Gln Pro Pro Ser Tyr Gly Pro Val Leu Ser Pro Met Asn Lys  
 405 410 415

*AS*  
 Val His Gly Gly Met Asn Lys Leu Pro Ser Val Asn Gln Leu Val Gly  
 420 425 430

*WT*  
 Gln Pro Pro Pro His Ser Ser Ala Ala Thr Pro Asn Leu Gly Pro Val  
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Gly Pro Gly Met Leu Asn Asn His Gly His Ala Val Pro Ala Asn Gly  
 450 455 460

Glu Met Ser Ser Ser His Ser Ala Gln Ser Met Val Ser Gly Ser His  
 465 470 475 480

Cys Thr Pro Pro Pro Tyr His Ala Asp Pro Ser Leu Val Ser Phe  
 485 490 495

Leu Thr Gly Leu Gly Cys Pro Asn Cys Ile Glu Tyr Phe Thr Ser Gln  
 500 505 510

Gly Leu Gln Ser Ile Tyr His Leu Gln Asn Leu Thr Ile Glu Asp Leu  
 515 520 525

Gly Ala Leu Lys Ile Pro Glu Gln Tyr Arg Met Thr Ile Trp Arg Gly  
 530 535 540

Leu Gln Asp Leu Lys Gln Gly His Asp Tyr Ser Thr Ala Gln Gln Leu  
 545 550 555 560

Leu Arg Ser Ser Asn Ala Ala Thr Ile Ser Ile Gly Gly Ser Gly Glu  
565 570 575

Leu Gln Arg Gln Arg Val Met Glu Ala Val His Phe Arg Val Arg His  
580 585 590

Thr Ile Thr Ile Pro Asn Arg Gly Gly Pro Gly Gly Pro Asp Glu  
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/   Met Cys Met Gly Pro Val Tyr Glu Ser Leu Gly Gln Ala Gln Phe
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AAT TTG CTC AGC AGT GCC ATG GAC CAG ATG GGC AGC CGT GCG GCC CCG 216  
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 Ala Ser Pro Tyr Thr Pro Glu His Ala Ala Ser Ala Pro Thr His Ser  
                  35                 40                 45

CCC TAC GCG CAG CCC AGC TCC ACC TTC GAC ACC ATG TCT CCG GCG CCT  
 Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Thr Met Ser Pro Ala Pro  
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GTC ATC CCT TCC AAT ACC GAC TAC CCC GGC CCC CAC CAC TTC GAG GTC  
 Val Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro His His Phe Glu Val  
                  65                 70                 75

ACC TTC CAG CAG TCG AGC ACT GCC AAG TCG GCC ACC TGG ACA TAC TCC 408  
 Thr Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala Thr Trp Thr Tyr Ser  
 80 85 90 95

CCA CTC TTG AAG AAG TTG TAC TGT CAG ATT GCT AAG ACA TGC CCC ATC 456

Pro Leu Leu Lys Lys Leu Tyr Cys Gln Ile Ala Lys Thr Cys Pro Ile			
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CAG ATC AAA GTG TCC ACA CCA CCA CCC CCG GGC ACG GCC ATC CGG GCC			504
Gln Ile Lys Val Ser Thr Pro Pro Pro Gly Thr Ala Ile Arg Ala			
115	120	125	
ATG CCT GTC TAC AAG AAG GCA GAG CAT GTG ACC GAC ATT GTT AAG CGC			552
Met Pro Val Tyr Lys Lys Ala Glu His Val Thr Asp Ile Val Lys Arg			
130	135	140	
TGC CCC AAC CAC GAG CTT GGA AGG GAC TTC AAT GAA GGA CAG TCT GCC			600
Cys Pro Asn His Glu Leu Gly Arg Asp Phe Asn Glu Gly Gln Ser Ala			
145	150	155	
CCG GCT AGC CAC CTC ATC CGT GTA GAA GGC AAC AAC CTC GCC CAG TAC			648
Pro Ala Ser His Leu Ile Arg Val Glu Gly Asn Asn Leu Ala Gln Tyr			
160	165	170	175
GTG GAT GAC CCT GTC ACC GGA AGG CAG AGT GTG GTT GTG CCG TAT GAA			696
Val Asp Asp Pro Val Thr Gly Arg Gln Ser Val Val Val Pro Tyr Glu			
180	185	190	
CCC CCA CAG GTG GGA ACA GAA TTT ACC ACC ATC CTG TAC AAC TTC ATG			744
Pro Pro Gln Val Gly Thr Glu Phe Thr Thr Ile Leu Tyr Asn Phe Met			
195	200	205	
TGT AAC AGC AGC TGT GTG GGG GGC ATG AAT CGG AGG CCC ATC CTT GTC			792
Cys Asn Ser Ser Cys Val Gly Gly Met Asn Arg Arg Pro Ile Leu Val			
210	215	220	
ATC ATC ACC CTG GAG ACC CGG GAT GGA CAG GTC CTG GGC CGC CGG TCT			840
Ile Ile Thr Leu Glu Thr Arg Asp Gly Gln Val Leu Gly Arg Arg Ser			
225	230	235	
TTC GAG GGT CGC ATC TGT GCC TGT CCT GGC CGT GAC CGC AAA GCT GAT			888
Phe Glu Gly Arg Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala Asp			
240	245	250	255
GAA GAC CAT TAC CGG GAG CAA CAG GCT CTG AAT GAA AGT ACC ACC AAA			936
Glu Asp His Tyr Arg Glu Gln Gln Ala Leu Asn Glu Ser Thr Thr Lys			
260	265	270	
AAT GGA GCT GCC AGC AAA CGT GCA TTC AAG CAG AGC CCC CCT GCC ATC			984
Asn Gly Ala Ala Ser Lys Arg Ala Phe Lys Gln Ser Pro Pro Ala Ile			
275	280	285	
CCT GCC CTG GGT ACC AAC GTG AAG AAG AGA CGC CAC GGG GAC GAG GAC			1032
Pro Ala Leu Gly Thr Asn Val Lys Lys Arg Arg His Gly Asp Glu Asp			
290	295	300	
ATG TTC TAC ATG CAC GTG CGA GGC CGG GAG AAC TTT GAG ATC TTG ATG			1080
Met Phe Tyr Met His Val Arg Gly Arg Glu Asn Phe Glu Ile Leu Met			
305	310	315	
AAA GTC AAG GAG AGC CTA GAA CTG ATG GAG CTT GTG CCC CAG CCT TTG			1128
Lys Val Lys Glu Ser Leu Glu Leu Met Glu Leu Val Pro Gln Pro Leu			

		19		
320	325	330		335
GTT GAC TCC TAT CGA CAG CAG CAG CAG CAG CTC CTA CAG AGG CCG Val Asp Ser Tyr Arg Gln Gln Gln Gln Gln Leu Leu Gln Arg Pro				1176
340	345		350	
AGT CAC CTG CAG CCT CCA TCC TAT GGG CCC GTG CTC TCC CCA ATG AAC Ser His Leu Gln Pro Pro Ser Tyr Gly Pro Val Leu Ser Pro Met Asn				1224
355	360		365	
AAG GTA CAC GGT GTC AAC AAA CTG CCC TCC GTC AAC CAG CTG GTG Lys Val His Gly Gly Val Asn Lys Leu Pro Ser Val Asn Gln Leu Val				1272
370	375		380	
GGC CAG CCT CCC CCG CAC AGC TCA GCA GCT GGG CCC AAC CTG GGG CCC Gly Gln Pro Pro Pro His Ser Ser Ala Ala Gly Pro Asn Leu Gly Pro				1320
385	390		395	
ATG GGC TCC GGG ATG CTC AAC AGC CAC GGC CAC AGC ATG CCG GCC AAT Met Gly Ser Gly Met Leu Asn Ser His Gly His Ser Met Pro Ala Asn				1368
400	405		410	415
GGT GAG ATG AAT GGA GGC CAC AGC TCC CAG ACC ATG GTT TCG GGA TCC Gly Glu Met Asn Gly Gly His Ser Ser Gln Thr Met Val Ser Gly Ser				1416
420	425		430	
CAC TGC ACC CCG CCA CCC CCC TAT CAT GCA GAC CCC AGC CTC GTC AGT His Cys Thr Pro Pro Pro Tyr His Ala Asp Pro Ser Leu Val Ser				1464
435	440		445	
AS W				
TTT TTG ACA GGG TTG GGG TGT CCA AAC TGC ATC GAG TGC TTC ACT TCC Phe Leu Thr Gly Leu Gly Cys Pro Asn Cys Ile Glu Cys Phe Thr Ser				1512
450	455		460	
CAA GGG TTG CAG AGC ATC TAC CAC CTG CAG AAC CTT ACC ATC GAG GAC Gln Gly Leu Gln Ser Ile Tyr His Leu Gln Asn Leu Thr Ile Glu Asp				1560
465	470		475	
CTT GGG GCT CTG AAG GTC CCT GAC CAG TAC CGT ATG ACC ATC TGG AGG Leu Gly Ala Leu Lys Val Pro Asp Gln Tyr Arg Met Thr Ile Trp Arg				1608
480	485		490	495
GGC CTA CAG GAC CTG AAG CAG AGC CAT GAC TGC GGC CAG CAA CTG CTA Gly Leu Gln Asp Leu Lys Gln Ser His Asp Cys Gly Gln Gln Leu Leu				1656
500	505		510	
CGC TCC AGC AGC AAC GCG GCC ACC ATC TCC ATC GGC GGC TCT GGC GAG Arg Ser Ser Ser Asn Ala Ala Thr Ile Ser Ile Gly Gly Ser Gly Glu				1704
515	520		525	
CTG CAG CGG CAG CGG GTC ATG GAA GCC GTG CAT TTC CGT GTG CGC CAC Leu Gln Arg Gln Arg Val Met Glu Ala Val His Phe Arg Val Arg His				1752
530	535		540	
ACC ATC ACA ATC CCC AAC CGT GGA GGC GCA GGT GCG GTG ACA GGT CCC Thr Ile Thr Ile Pro Asn Arg Gly Gly Ala Gly Ala Val Thr Gly Pro				1800
545	550		555	

GAC GAG TGG GCG GAC TTT GGC TTT GAC CTG CCT GAC TGC AAG TCC CGT		1848	
Asp Glu Trp Ala Asp Phe Gly Phe Asp Leu Pro Asp Cys Lys Ser Arg			
560	565	570	575
AAG CAG CCC ATC AAA GAG GAG TTC ACA GAG ACA GAG AGC CAC		1890	
Lys Gln Pro Ile Lys Glu Glu Phe Thr Glu Thr Glu Ser His			
580	585		
TGAGGAACGT ACCTTCTTCT CCTGTCCTTC CTCTGTGAGA AACTGCTCTT GGAAGTGGGA		1950	
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Ser Pro Tyr Thr Pro Glu His Ala Ala Ser Ala Pro Thr His Ser Pro			
35	40	45	

<i>AS</i>	Tyr Ala Gln Pro Ser Ser Thr Phe Asp Thr Met Ser Pro Ala Pro Val		
50	55	60	

Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro His His Phe Glu Val Thr			
65	70	75	80

Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala Thr Trp Thr Tyr Ser Pro			
85	90	95	

Leu Leu Lys Lys Leu Tyr Cys Gln Ile Ala Lys Thr Cys Pro Ile Gln			
100	105	110	

Ile Lys Val Ser Thr Pro Pro Pro Gly Thr Ala Ile Arg Ala Met			
115	120	125	

Pro Val Tyr Lys Lys Ala Glu His Val Thr Asp Ile Val Lys Arg Cys			
130	135	140	

Pro Asn His Glu Leu Gly Arg Asp Phe Asn Glu Gly Gln Ser Ala Pro			
145	150	155	160

Ala Ser His Leu Ile Arg Val Glu Gly Asn Asn Leu Ala Gln Tyr Val			
165	170	175	

Asp Asp Pro Val Thr Gly Arg Gln Ser Val Val Val Pro Tyr Glu Pro  
 180 185 190

Pro Gln Val Gly Thr Glu Phe Thr Thr Ile Leu Tyr Asn Phe Met Cys  
 195 200 205

Asn Ser Ser Cys Val Gly Gly Met Asn Arg Arg Pro Ile Leu Val Ile  
 210 215 220

Ile Thr Leu Glu Thr Arg Asp Gly Gln Val Leu Gly Arg Arg Ser Phe  
 225 230 235 240

Glu Gly Arg Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala Asp Glu  
 245 250 255

Asp His Tyr Arg Glu Gln Gln Ala Leu Asn Glu Ser Thr Thr Lys Asn  
 260 265 270

Gly Ala Ala Ser Lys Arg Ala Phe Lys Gln Ser Pro Pro Ala Ile Pro  
 275 280 285

Ala Leu Gly Thr Asn Val Lys Lys Arg Arg His Gly Asp Glu Asp Met  
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Phe Tyr Met His Val Arg Gly Arg Glu Asn Phe Glu Ile Leu Met Lys  
 305 310 315 320

Val Lys Glu Ser Leu Glu Leu Met Glu Leu Val Pro Gln Pro Leu Val  
 325 330 335

Asp Ser Tyr Arg Gln Gln Gln Gln Gln Leu Leu Gln Arg Pro Ser  
 340 345 350

His Leu Gln Pro Pro Ser Tyr Gly Pro Val Leu Ser Pro Met Asn Lys  
 355 360 365

Val His Gly Gly Val Asn Lys Leu Pro Ser Val Asn Gln Leu Val Gly  
 370 375 380

Gln Pro Pro Pro His Ser Ser Ala Ala Gly Pro Asn Leu Gly Pro Met  
 385 390 395 400

Gly Ser Gly Met Leu Asn Ser His Gly His Ser Met Pro Ala Asn Gly  
 405 410 415

Glu Met Asn Gly Gly His Ser Ser Gln Thr Met Val Ser Gly Ser His  
 420 425 430

Cys Thr Pro Pro Pro Tyr His Ala Asp Pro Ser Leu Val Ser Phe  
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Leu Thr Gly Leu Gly Cys Pro Asn Cys Ile Glu Cys Phe Thr Ser Gln  
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Gly Leu Gln Ser Ile Tyr His Leu Gln Asn Leu Thr Ile Glu Asp Leu  
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Gly Ala Leu Lys Val Pro Asp Gln Tyr Arg Met Thr Ile Trp Arg Gly  
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Leu Gln Asp Leu Lys Gln Ser His Asp Cys Gly Gln Gln Leu Leu Arg  
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Ser Ser Ser Asn Ala Ala Thr Ile Ser Ile Gly Gly Ser Gly Glu Leu  
 515 520 525

Gln Arg Gln Arg Val Met Glu Ala Val His Phe Arg Val Arg His Thr  
 530 535 540

Ile Thr Ile Pro Asn Arg Gly Gly Ala Gly Ala Val Thr Gly Pro Asp  
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Glu Trp Ala Asp Phe Gly Phe Asp Leu Pro Asp Cys Lys Ser Arg Lys  
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GGGCCCGAGA CCCCGACTCG GGCAGAGCCA GCTGGGGAGG CGGGGCGCGC GTGGGAGCCA	180
GGGGCCCCGGG TGGCCGGCCC TCCTCCGCCA CGGCTGAGTG CCCGCGCTGC CTTCCCGCCG	240
GTCCGCCAAG AAAGGCCTA AGCCTGCGGC AGTCCCCTCG CCGCCGCCTC CCTGCTCCGC	300
ACCCCTTATAA CCCGCCGTCC CGCATCCAGG CGAGGAGGCA ACGCTGCAGC CCAGCCCTCG	360
CCGACGCCGA CGCCCGGCC CGAGCAGA ATG AGC GGC AGC GTT GGG GAG ATG Met Ser Gly Ser Val Gly Glu Met	412
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TCT CTA GAG CCA GAC ACC TAC TTT GAC CTC CCC CAG CCC AGC CAA Ser Leu Glu Pro Asp Ser Thr Tyr Phe Asp Leu Pro Gln Pro Ser Gln	508
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GGG ACT AGC GAG GCA TCA GGC AGC GAG GAG TCC AAC ATG GAT GTC TTC	556
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Gly Thr Ser Glu Ala Ser Gly Ser Glu Glu Ser Asn Met Asp Val Phe  
 45 50 55

CAC CTG CAA GGC ATG GCC CAG TTC AAT TTG CTC AGC AGT GCC ATG GAC 604  
 His Leu Gln Gly Met Ala Gln Phe Asn Leu Leu Ser Ser Ala Met Asp  
 60 65 70

CAG ATG GGC AGC CGT GCG GCC CCG GCG AGC CCC TAC ACC ACC CCG GAG CAC 652  
 Gln Met Gly Ser Arg Ala Ala Pro Ala Ser Pro Tyr Thr Pro Glu His  
 75 80 85

GCC GCC AGC GCG CCC ACC CAC TCG CCC TAC GCG CAG CCC AGC TCC ACC 700  
 Ala Ala Ser Ala Pro Thr His Ser Pro Tyr Ala Gln Pro Ser Ser Thr  
 90 95 100

TTC GAC ACC ATG TCT CCG GCG CCT GTC ATC CCT TCC AAT ACC GAC TAC 748  
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CCC GGC CCC C 758  
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Glu Glu Ser Asn Met Asp Val Phe His Leu Gln Gly Met Ala Gln Phe  
 50 55 60

Asn Leu Leu Ser Ser Ala Met Asp Gln Met Gly Ser Arg Ala Ala Pro  
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Ala Ser Pro Tyr Thr Pro Glu His Ala Ala Ser Ala Pro Thr His Ser  
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GGACGTCTTC CACCTGGAGG GCATGACTAC ATCTGTCAAT CATCCTCGGC TCCTGCCCTCA	120
CTAGCTGCGG AGCCTCTCCC GCTCGGTCCA CGCTGCCGGG CGGCCACGAC CGTGACCCTT	180
CCCCCTGGGC CGCCCAGATC CATGCCTCGT CCCACGGGAC ACCAGTTCCC TGGCGTGTGC	240
AGACCCCCCG GCGCCTACCA TGCTGTACGT CGGTGACCCCC GCACGGCACC TCGCCACGGC	300
CCAGTTCAAT CTGCTGAGCA GCACCATGGA CCAGATGAGC AGCCGCGCGG CCTCGGCCAG	360
CCCCCTACACC CCAGAGCACG CCGCCAGCGT GCCCACCCAC TCGCCCTACG CACAACCCAG	420
CTCCACCTTC GACACCATGT CGCCGGCGCC TGTCATCCCC TCCAACACCG ACTACCCCGG	480
ACCCCCACCAC TTTGAGGTCA CTTTCCAGCA GTCCAGCACG GCCAAGTCAG CCACCTGGAC	540
GTACTCCCCG CTCTTGAAG	559

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GCCGCCAGCG TGCCCACCCA CTCGCCCTAC GCACAACCCA GCTCCACCTT CGACACCATG	180
TCGCCGGCGC CTGTCATCCC CTCCAACACC GACTACCCCG GACCCCACCA CTTTGAGGTC	240
ACTTTCCAGC AGTCCAGCAC GGCCAAGTCA GCCACCTGGA CGTACTCCCC GCTCTTGAAG	300
AAACTCTACT GCCAGATCGC CAAGACATGC CCCATCCAGA TCAAGGTGTC CACCCGCCA	360
CCCCCAGGCA CTGCCATCCG GGCCATGCCT GTTTACAAGA AAGCGGAGCA CGTGACCGAC	420
GTCGTGAAAC GCTGCCCAA CCACGAGCTC GGGAGGGACT TCAACGAAGG ACAGTCTGCT	480
CCAGCCAGCC ACCTCATCCG CGTGGAAAGGC AATAATCTCT CGCAGTATGT GGATGACCCT	540
GTCACCGGCA GGCAGAGCGT CGTGGTGCCT TATGAGCCAC CACAGGTGGG GACGGAATTG	600
ACCACCATCC TGTACAACCTT CATGTGTAAC AGCAGCTGTG TAGGGGGCAT GAACCGGGCGG	660

25

CCCATCCTCA	TCATCATCAC	CCTGGAGATG	CGGGATGGC	AGGTGCTGGG	CCGCCGGTCC	720
TTTGAGGGCC	GCATCTGCGC	CTGTCCTGGC	CGCGACCGAA	AAGCTGATGA	GGACCACTAC	780
CGGGAGCAGC	AGGCCCTGAA	CGAGAGCTCC	GCCAAGAACG	GGGCCGCCAG	CAAGCGTGCC	840
TTCAAGCAGA	GCCCCCTGCG	CGTCCCCGCC	CTTGGTGCCG	GTGTGAAGAA	GCGGCGGCAT	900
GGAGACGAGG	ACACGTACTA	CCTTCAGGTG	CGAGGCCGGG	AGAACTTTGA	GATCCTGATG	960
AAGCTGAAAG	AGAGCCTGGA	GCTGATGGAG	TTGGTGCCGC	AGCCACTGGT	GGACTCCTAT	1020
CGGCAGCAGC	AGCAGCTCCT	ACAGAGGCCG	AGTCACCTAC	AGCCCCCGTC	CTACGGGCCG	1080
GTCCTCTCGC	CCATGAACAA	GGTGCACGGG	GGCATGAACA	AGCTGCCCTC	CGTCAACCAG	1140
CTGGTGGGCC	AGCCTCCCCC	GCACAGTTCG	GCAGCTACAC	CCAACCTGGG	GCCCCTGGGC	1200
CCCGGGATGC	TCAACAACCA	TGGCCACGCA	GTGCCAGCCA	ACGGCGAGAT	GAGCAGCAGC	1260
CACAGCGCCC	AGTCCATGGT	CTCGGGGTCC	CACTGCACTC	CGCCACCCCC	CTACCACGCC	1320
GACCCCAGCC	TCGTCAGTTT	TTAACAGGA	TTGGGGTGTC	CAAAC TGCA	CGAGTATTTC	1380
ACCTCCCAAG	GGTTACAGAG	CATTTACAC	CTGCAGAAC	TGACCATTGA	GGACCTGGGG	1440
GCCCTGAAGA	TCCCCGAGCA	GTACCGCATG	ACCATCTGGC	GGGGCCTGCA	GGACCTGAAG	1500
CAGGGCCACG	ACTACAGCAC	CGCGCAGCAG	CTGCTCCGCT	CTAGCAACGC	GGCCACCATC	1560
TCCATCGGCG	GCTCAGGGGA	ACTGCAGCGC	CAGCGGTCA	TGGAGGCCGT	GCACTTCCGC	1620
GTGCGCCACA	CCATCACCAT	CCCCAACCGC	GGCGGCCAG	GCGGCGGCC	TGACGAGTGG	1680
GCGGACTTCG	GCTTCGACCT	GCCGACTGC	AAGGCCGCA	AGCAGCCC	CAAGGAGGAG	1740
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Ala Ser Pro Tyr Thr Pro Glu His Ala Ala Ser Val Pro Thr His Ser  
 35 40 45

Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Thr Met Ser Pro Ala Pro  
 50 55 60

Val Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro His His Phe Glu Val  
 65 70 75 80

Thr Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala Thr Trp Thr Tyr Ser  
 85 90 95

Pro Leu Leu Lys Lys Leu Tyr Cys Gln Ile Ala Lys Thr Cys Pro Ile  
 100 105 110

Gln Ile Lys Val Ser Thr Pro Pro Pro Gly Thr Ala Ile Arg Ala  
 115 120 125

Met Pro Val Tyr Lys Lys Ala Glu His Val Thr Asp Val Val Lys Arg  
 130 135 140

Cys Pro Asn His Glu Leu Gly Arg Asp Phe Asn Glu Gly Gln Ser Ala  
 145 150 155 160

Pro Ala Ser His Leu Ile Arg Val Glu Gly Asn Asn Leu Ser Gln Tyr  
 165 170 175

Val Asp Asp Pro Val Thr Gly Arg Gln Ser Val Val Val Pro Tyr Glu  
 180 185 190

Pro Pro Gln Val Gly Thr Glu Phe Thr Thr Ile Leu Tyr Asn Phe Met  
 195 200 205

Cys Asn Ser Ser Cys Val Gly Gly Met Asn Arg Arg Pro Ile Leu Ile  
 210 215 220


 Ile Ile Thr Leu Glu Met Arg Asp Gly Gln Val Leu Gly Arg Arg Ser  
 225 230 235 240

Phe Glu Gly Arg Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala Asp  
 245 250 255

Glu Asp His Tyr Arg Glu Gln Gln Ala Leu Asn Glu Ser Ser Ala Lys  
 260 265 270

Asn Gly Ala Ala Ser Lys Arg Ala Phe Lys Gln Ser Pro Pro Ala Val  
 275 280 285

Pro Ala Leu Gly Ala Gly Val Lys Lys Arg Arg His Gly Asp Glu Asp  
 290 295 300

Thr Tyr Tyr Leu Gln Val Arg Gly Arg Glu Asn Phe Glu Ile Leu Met  
 305 310 315 320

Lys Leu Lys Glu Ser Leu Glu Leu Met Glu Leu Val Pro Gln Pro Leu  
 325 330 335

Val Asp Ser Tyr Arg Gln Gln Gln Leu Leu Gln Arg Pro Ser His  
 340 345 350

Leu Gln Pro Pro Ser Tyr Gly Pro Val Leu Ser Pro Met Asn Lys Val  
 355 360 365

His Gly Gly Met Asn Lys Leu Pro Ser Val Asn Gln Leu Val Gly Gln  
370 375 380

Pro Pro Pro His Ser Ser Ala Ala Thr Pro Asn Leu Gly Pro Val Gly  
385 390 395 400

Pro Gly Met Leu Asn Asn His Gly His Ala Val Pro Ala Asn Gly Glu  
405 410 415

Met Ser Ser Ser His Ser Ala Gln Ser Met Val Ser Gly Ser His Cys  
420 425 430

Thr Pro Pro Pro Tyr His Ala Asp Pro Ser Leu Val Ser Phe Leu  
435 440 445

Thr Gly Leu Gly Cys Pro Asn Cys Ile Glu Tyr Phe Thr Ser Gln Gly  
450 455 460

Leu Gln Ser Ile Tyr His Leu Gln Asn Leu Thr Ile Glu Asp Leu Gly  
465 470 475 480

Ala Leu Lys Ile Pro Glu Gln Tyr Arg Met Thr Ile Trp Arg Gly Leu  
485 490 495

Gln Asp Leu Lys Gln Gly His Asp Tyr Ser Thr Ala Gln Gln Leu Leu  
500 505 510

Arg Ser Ser Asn Ala Ala Thr Ile Ser Ile Gly Gly Ser Gly Glu Leu  
515 520 525

Gln Arg Gln Arg Val Met Glu Ala Val His Phe Arg Val Arg His Thr  
530 535 540

Ile Thr Ile Pro Asn Arg Gly Gly Pro Gly Gly Gly Pro Asp Glu Trp  
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Ala Asp Phe Gly Phe Asp Leu Pro Asp Cys Lys Ala Arg Lys Gln Pro  
565 570 575

Ile Lys Glu Glu Phe Thr Glu Ala Glu Ile His  
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TCGCCGGCGC	CTGTCATCCC	CTCCAACACC	GACTACCCCG	GACCCCCACCA	CTTTGAGGTC	240
ACTTTCCAGC	AGTCCAGCAC	GGCCAAGTCA	GCCACCTGGA	CGTACTCCCC	GCTCTTGAAG	300
AAACTCTACT	GCCAGATCGC	CAAGACATGC	CCCATCCAGA	TCAAGGTGTC	CACCCCGCCA	360
CCCCCAGGCA	CTGCCATCCG	GGCCATGCCT	GTTCACAAGA	AAGCGGAGCA	CGTGACCGAC	420
GTCGTGAAAC	GCTGCCCAA	CCACGAGCTC	GGGAGGGACT	TCAACGAAGG	ACAGTCTGCT	480
CCAGCCAGCC	ACCTCATCCG	CGTGGAAAGGC	AATAATCTCT	CGCAGTATGT	GGATGACCCT	540
GTCACCGGCA	GGCAGAGCGT	CGTGGTGCCT	TATGAGCCAC	CACAGGTGGG	GACGGAATTG	600
ACCACCATCC	TGTACAACTT	CATGTGTAAC	AGCAGCTGTG	TAGGGGGCAT	GAACCGGCGG	660
CCCATCCTCA	TCATCATCAC	CCTGGAGATG	CGGGATGGC	AGGTGCTGGG	CCGCCGGTCC	720
TTTGAGGGCC	GCATCTGCGC	CTGTCCTGGC	CGCGACCGAA	AAGCTGATGA	GGACCACTAC	780
CGGGAGCAGC	AGGCCCTGAA	CGAGAGCTCC	GCCAAGAACG	GGGCCGCCAG	CAAGCGTGCC	840
TTCAAGCAGA	GCCCCCTGC	CGTCCCCGCC	CTTGGTGCCTG	GTGTGAAGAA	GCGGCGGCAT	900
GGAGACGAGG	ACACGTACTA	CCTTCAGGTG	CGAGGCCGGG	AGAACTTTGA	GATCCTGATG	960
AAGCTGAAAG	AGAGCCTGGA	GCTGATGGAG	TTGGTGCCTGC	AGCCACTGGT	GGACTCCTAT	1020
CGGCAGCAGC	AGCAGCTCCT	ACAGAGGCCG	CCCCGGGATG	CTCAACAAACC	ATGGCCACGC	1080
AGTGCCAGCC	AACGGCGAGA	TGAGCAGCAG	CCACAGCGCC	CAGTCCATGG	TCTCGGGGTC	1140
CCACTGCACT	CCGCCACCCC	CCTACCACGC	CGACCCCAGC	CTCGTCAGGA	CCTGGGGGCC	1200
CTGAAGATCC	CCGAGCAGTA	CCGCATGACC	ATCTGGCGGG	GCCTGCAGGA	CCTGAAGCAG	1260
GGCCACGACT	ACAGCACCGC	GCAGCAGCTG	CTCCGCTCTA	GCAACGCGGC	CACCATCTCC	1320
ATCGGCGGCT	CAGGGGAAC	GCAGCGCCAG	CGGGTCATGG	AGGCCGTGCA	CTTCCGCGTG	1380
CGCCACACCA	TCACCATCCC	CAACCGCGGC	GGCCCAGGCG	GCGGCCCTGA	CGAGTGGGCG	1440
GACTTCGGCT	TCGACCTGCC	CGACTGCAAG	GCCCCGAAGC	AGCCCATCAA	GGAGGAGTTC	1500
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Asn Leu Leu Ser Ser Thr Met Asp Gln Met Ser Ser Arg Ala Ala Ser  
 20 25 30

Ala Ser Pro Tyr Thr Pro Glu His Ala Ala Ser Val Pro Thr His Ser  
 35 40 45

Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Thr Met Ser Pro Ala Pro  
 50 55 60

Val Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro His His Phe Glu Val  
 65 70 75 80

Thr Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala Thr Trp Thr Tyr Ser  
 85 90 95

Pro Leu Leu Lys Lys Leu Tyr Cys Gln Ile Ala Lys Thr Cys Pro Ile  
 100 105 110

Gln Ile Lys Val Ser Thr Pro Pro Pro Pro Gly Thr Ala Ile Arg Ala  
 115 120 125

Met Pro Val Tyr Lys Lys Ala Glu His Val Thr Asp Val Val Lys Arg  
 130 135 140

Cys Pro Asn His Glu Leu Gly Arg Asp Phe Asn Glu Gly Gln Ser Ala  
 145 150 155 160

Pro Ala Ser His Leu Ile Arg Val Glu Gly Asn Asn Leu Ser Gln Tyr  
 165 170 175

Val Asp Asp Pro Val Thr Gly Arg Gln Ser Val Val Val Pro Tyr Glu  
 180 185 190

Pro Pro Gln Val Gly Thr Glu Phe Thr Thr Ile Leu Tyr Asn Phe Met  
 195 200 205

Cys Asn Ser Ser Cys Val Gly Gly Met Asn Arg Arg Pro Ile Leu Ile  
 210 215 220

Ile Ile Thr Leu Glu Met Arg Asp Gly Gln Val Leu Gly Arg Arg Ser  
 225 230 235 240

Phe Glu Gly Arg Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala Asp  
 245 250 255

Glu Asp His Tyr Arg Glu Gln Gln Ala Leu Asn Glu Ser Ser Ala Lys  
 260 265 270

Asn Gly Ala Ala Ser Lys Arg Ala Phe Lys Gln Ser Pro Pro Ala Val  
 275 280 285

Pro Ala Leu Gly Ala Gly Val Lys Lys Arg Arg His Gly Asp Glu Asp  
 290 295 300

Thr Tyr Tyr Leu Gln Val Arg Gly Arg Glu Asn Phe Glu Ile Leu Met  
 305 310 315 320

30

Lys Leu Lys Glu Ser Leu Glu Leu Met Glu Leu Val Pro Gln Pro Leu  
325 330 335

Val Asp Ser Tyr Arg Gln Gln Gln Leu Leu Gln Arg Pro Pro Arg  
340 345 350

Asp Ala Gln Gln Pro Trp Pro Arg Ser Ala Ser Gln Arg Arg Asp Glu  
355 360 365

Gln Gln Pro Gln Arg Pro Val His Gly Leu Gly Val Pro Leu His Ser  
370 375 380

Ala Thr Pro Leu Pro Arg Arg Pro Gln Pro Arg Gln Asp Leu Gly Ala  
385 390 395 400

Leu Lys Ile Pro Glu Gln Tyr Arg Met Thr Ile Trp Arg Gly Leu Gln  
405 410 415

Asp Leu Lys Gln Gly His Asp Tyr Ser Thr Ala Gln Gln Leu Leu Arg  
420 425 430

Ser Ser Asn Ala Ala Thr Ile Ser Ile Gly Gly Ser Gly Glu Leu Gln  
435 440 445

Arg Gln Arg Val Met Glu Ala Val His Phe Arg Val Arg His Thr Ile  
450 455 460

Thr Ile Pro Asn Arg Gly Gly Pro Gly Gly Pro Asp Glu Trp Ala  
465 470 475 480

Asp Phe Gly Phe Asp Leu Pro Asp Cys Lys Ala Arg Lys Gln Pro Ile  
485 490 495

Lys Glu Glu Phe Thr Glu Ala Glu Ile His  
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Cwt  
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<400> 16

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Met Asp Val Phe  
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CAC CTG GAG GGC ATG ACT ACA TCT GTC ATG GCC CAG TTC AAT CTG CTG 163  
His Leu Glu Gly Met Thr Thr Ser Val Met Ala Gln Phe Asn Leu Leu  
5 10 15 20

AGC AGC ACC ATG GAC CAG ATG AGC AGC CGC GCG GCC TCG GCC AGC CCC 211

Ser Ser Thr Met Asp Gln Met Ser Ser Arg Ala Ala Ser Ala Ser Pro			
25	30	35	
TAC ACC CCA GAG CAC GCC GCC AGC GTG CCC ACC CAC TCG CCC TAC GCA			
Tyr Thr Pro Glu His Ala Ala Ser Val Pro Thr His Ser Pro Tyr Ala			
40	45	50	259
CAA CCC AGC TCC ACC TTC GAC ACC ATG TCG CCG GCG CCT GTC ATC CCC			
Gln Pro Ser Ser Thr Phe Asp Thr Met Ser Pro Ala Pro Val Ile Pro			
55	60	65	307
TCC AAC ACC GAC TAC CCC GGA CCC CAC CAC TTT GAG GTC ACT TTC CAG			
Ser Asn Thr Asp Tyr Pro Gly Pro His His Phe Glu Val Thr Phe Gln			
70	75	80	355
CAG TCC AGC ACG GCC AAG TCA GCC ACC TGG ACG TAC TCC CCG CTC TTG			
Gln Ser Ser Thr Ala Lys Ser Ala Thr Trp Thr Tyr Ser Pro Leu Leu			
85	90	95	100
AAG AAA CTC TAC TGC CAG ATC GCC AAG ACA TGC CCC ATC CAG ATC AAG			
Lys Lys Leu Tyr Cys Gln Ile Ala Lys Thr Cys Pro Ile Gln Ile Lys			
105	110	115	403
GTG TCC ACC CCG CCA CCC CCA GGC ACT GCC ATC CGG GCC ATG CCT GTT			
Val Ser Thr Pro Pro Pro Pro Gly Thr Ala Ile Arg Ala Met Pro Val			
120	125	130	499
TAC AAG AAA GCG GAG CAC GTG ACC GAC GTC GTG AAA CGC TGC CCC AAC			
Tyr Lys Lys Ala Glu His Val Thr Asp Val Val Lys Arg Cys Pro Asn			
135	140	145	547
CAC GAG CTC GGG AGG GAC TTC AAC GAA GGA CAG TCT GCT CCA GCC AGC			
His Glu Leu Gly Arg Asp Phe Asn Glu Gly Gln Ser Ala Pro Ala Ser			
150	155	160	595
CAC CTC ATC CGC GTG GAA GGC AAT AAT CTC TCG CAG TAT GTG GAT GAC			
His Leu Ile Arg Val Glu Gly Asn Asn Leu Ser Gln Tyr Val Asp Asp			
165	170	175	180
CCT GTC ACC GGC AGG CAG AGC GTC GTG GTG CCC TAT GAG CCA CCA CAG			
Pro Val Thr Gly Arg Gln Ser Val Val Val Pro Tyr Glu Pro Pro Gln			
185	190	195	643
GTG GGG ACG GAA TTC ACC ACC ATC CTG TAC AAC TTC ATG TGT AAC AGC			
Val Gly Thr Glu Phe Thr Thr Ile Leu Tyr Asn Phe Met Cys Asn Ser			
200	205	210	691
AGC TGT GTA GGG GGC ATG AAC CGG CGG CCC ATC CTC ATC ATC ATC ACC			
Ser Cys Val Gly Gly Met Asn Arg Arg Pro Ile Leu Ile Ile Ile Thr			
215	220	225	787
CTG GAG ATG CGG GAT GGG CAG GTG CTG GGC CGC CGG TCC TTT GAG GGC			
Leu Glu Met Arg Asp Gly Gln Val Leu Gly Arg Arg Ser Phe Glu Gly			
230	235	240	835
CGC ATC TGC GCC TGT CCT GGC CGC GAC CGA AAA GCT GAT GAG GAC CAC			
Arg Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala Asp Glu Asp His			
			883

		32		
245	250	255		260
TAC CGG GAG CAG CAG GCC CTG AAC GAG AGC TCC GCC AAG AAC GGG GCC Tyr Arg Glu Gln Gln Ala Leu Asn Glu Ser Ser Ala Lys Asn Gly Ala 265		270		275
GCC AGC AAG CGT GCC TTC AAG CAG AGC CCC CCT GCC GTC CCC GCC CTT Ala Ser Lys Arg Ala Phe Lys Gln Ser Pro Pro Ala Val Pro Ala Leu 280		285		290
GGT GCC GGT GTG AAG AAG CGG CGG CAT GGA GAC GAG GAC ACG TAC TAC Gly Ala Gly Val Lys Lys Arg Arg His Gly Asp Glu Asp Thr Tyr Tyr 295		300		305
CTT CAG GTG CGA GGC CGG GAG AAC TTT GAG ATC CTG ATG AAG CTG AAA Leu Gln Val Arg Gly Arg Glu Asn Phe Glu Ile Leu Met Lys Leu Lys 310		315		320
GAG AGC CTG GAG CTG ATG GAG TTG GTG CCG CAG CCA CTG GTG GAC TCC Glu Ser Leu Glu Leu Met Glu Leu Val Pro Gln Pro Leu Val Asp Ser 325		330		335
TAT CGG CAG CAG CAG CAG CTC CTA CAG AGG CCG AGT CAC CTA CAG CCC Tyr Arg Gln Gln Gln Leu Leu Gln Arg Pro Ser His Leu Gln Pro 345		350		355
CCG TCC TAC GGG CCG GTC CTC TCG CCC ATG AAC AAG GTG CAC GGG GGC Pro Ser Tyr Gly Pro Val Leu Ser Pro Met Asn Lys Val His Gly Gly 360		365		370
ATG AAC AAG CTG CCC TCC GTC AAC CAG CTG GTG GGC CAG CCT CCC CCG Met Asn Lys Leu Pro Ser Val Asn Gln Leu Val Gly Gln Pro Pro Pro 375		380		385
CAC AGT TCG GCA GCT ACA CCC AAC CTG GGG CCC GTG GGC CCC GGG ATG His Ser Ser Ala Ala Thr Pro Asn Leu Gly Pro Val Gly Pro Gly Met 390		395		400
CTC AAC AAC CAT GGC CAC GCA GTG CCA GCC AAC GGC GAG ATG AGC AGC Leu Asn Asn His Gly His Ala Val Pro Ala Asn Gly Glu Met Ser Ser 405		410		415
AGC CAC AGC GCC CAG TCC ATG GTC TCG GGG TCC CAC TGC ACT CCG CCA Ser His Ser Ala Gln Ser Met Val Ser Gly Ser His Cys Thr Pro Pro 425		430		435
CCC CCC TAC CAC GCC GAC CCC AGC CTC GTC AGT TTT TTA ACA GGA TTG Pro Pro Tyr His Ala Asp Pro Ser Leu Val Ser Phe Leu Thr Gly Leu 440		445		450
GGG TGT CCA AAC TGC ATC GAG TAT TTC ACC TCC CAA GGG TTA CAG AGC Gly Cys Pro Asn Cys Ile Glu Tyr Phe Thr Ser Gln Gly Leu Gln Ser 455		460		465
ATT TAC CAC CTG CAG AAC CTG ACC ATT GAG GAC CTG GGG GCC CTG AAG Ile Tyr His Leu Gln Asn Leu Thr Ile Glu Asp Leu Gly Ala Leu Lys 470		475		480

ATC CCC GAG CAG TAC CGC ATG ACC ATC TGG CGG GGC CTG CAG GAC CTG Ile Pro Glu Gln Tyr Arg Met Thr Ile Trp Arg Gly Leu Gln Asp Leu 485 490 495 500	1603
AAG CAG GGC CAC GAC TAC AGC ACC GCG CAG CAG CTG CTC CGC TCT AGC Lys Gln Gly His Asp Tyr Ser Thr Ala Gln Gln Leu Leu Arg Ser Ser 505 510 515	1651
AAC GCG GCC ACC ATC TCC ATC GGC GGC TCA GGG GAA CTG CAG CGC CAG Asn Ala Ala Thr Ile Ser Ile Gly Gly Ser Gly Glu Leu Gln Arg Gln 520 525 530	1699
CGG GTC ATG GAG GCC GTG CAC TTC CGC GTG CGC CAC ACC ATC ACC ACC ATC Arg Val Met Glu Ala Val His Phe Arg Val Arg His Thr Ile Thr Ile 535 540 545	1747
CCC AAC CGC GGC GGC CCA GGC GGC CCT GAC GAG TGG GCG GAC TTC Pro Asn Arg Gly Gly Pro Gly Gly Pro Asp Glu Trp Ala Asp Phe 550 555 560	1795
GGC TTC GAC CTG CCC GAC TGC AAG GCC CGC AAG CAG CCC ATC AAG GAG Gly Phe Asp Leu Pro Asp Cys Lys Ala Arg Lys Gln Pro Ile Lys Glu 565 570 575 580	1843
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*W*

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Ser Ala Ser Pro Tyr Thr Pro Glu His Ala Ala Ser Val Pro Thr His 35 40 45	
Ser Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Thr Met Ser Pro Ala 50 55 60	
Pro Val Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro His His Phe Glu 65 70 75 80	
Val Thr Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala Thr Trp Thr Tyr 85 90 95	
Ser Pro Leu Leu Lys Lys Leu Tyr Cys Gln Ile Ala Lys Thr Cys Pro 100 105 110	

Ile Gln Ile Lys Val Ser Thr Pro Pro Pro Pro Gly Thr Ala Ile Arg  
 115 120 125

Ala Met Pro Val Tyr Lys Lys Ala Glu His Val Thr Asp Val Val Lys  
 130 135 140

Arg Cys Pro Asn His Glu Leu Gly Arg Asp Phe Asn Glu Gly Gln Ser  
 145 150 155 160

Ala Pro Ala Ser His Leu Ile Arg Val Glu Gly Asn Asn Leu Ser Gln  
 165 170 175

Tyr Val Asp Asp Pro Val Thr Gly Arg Gln Ser Val Val Val Pro Tyr  
 180 185 190

Glu Pro Pro Gln Val Gly Thr Glu Phe Thr Thr Ile Leu Tyr Asn Phe  
 195 200 205

Met Cys Asn Ser Ser Cys Val Gly Gly Met Asn Arg Arg Pro Ile Leu  
 210 215 220

Ile Ile Ile Thr Leu Glu Met Arg Asp Gly Gln Val Leu Gly Arg Arg  
 225 230 235 240

Ser Phe Glu Gly Arg Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala  
 245 250 255

Asp Glu Asp His Tyr Arg Glu Gln Gln Ala Leu Asn Glu Ser Ser Ala  
 260 265 270

Lys Asn Gly Ala Ala Ser Lys Arg Ala Phe Lys Gln Ser Pro Pro Ala  
 275 280 285

Val Pro Ala Leu Gly Ala Gly Val Lys Lys Arg Arg His Gly Asp Glu  
 290 295 300

Asp Thr Tyr Tyr Leu Gln Val Arg Gly Arg Glu Asn Phe Glu Ile Leu  
 305 310 315 320

Met Lys Leu Lys Glu Ser Leu Glu Leu Met Glu Leu Val Pro Gln Pro  
 325 330 335

Leu Val Asp Ser Tyr Arg Gln Gln Gln Leu Leu Gln Arg Pro Ser  
 340 345 350

His Leu Gln Pro Pro Ser Tyr Gly Pro Val Leu Ser Pro Met Asn Lys  
 355 360 365

Val His Gly Gly Met Asn Lys Leu Pro Ser Val Asn Gln Leu Val Gly  
 370 375 380

Gln Pro Pro Pro His Ser Ser Ala Ala Thr Pro Asn Leu Gly Pro Val  
 385 390 395 400

Gly Pro Gly Met Leu Asn Asn His Gly His Ala Val Pro Ala Asn Gly  
 405 410 415

AS  
WT

Glu Met Ser Ser Ser His Ser Ala Gln Ser Met Val Ser Gly Ser His  
420 425 430

Cys Thr Pro Pro Pro Tyr His Ala Asp Pro Ser Leu Val Ser Phe  
435 440 445

Leu Thr Gly Leu Gly Cys Pro Asn Cys Ile Glu Tyr Phe Thr Ser Gln  
450 455 460

Gly Leu Gln Ser Ile Tyr His Leu Gln Asn Leu Thr Ile Glu Asp Leu  
465 470 475 480

Gly Ala Leu Lys Ile Pro Glu Gln Tyr Arg Met Thr Ile Trp Arg Gly  
485 490 495

Leu Gln Asp Leu Lys Gln Gly His Asp Tyr Ser Thr Ala Gln Gln Leu  
500 505 510

Leu Arg Ser Ser Asn Ala Ala Thr Ile Ser Ile Gly Gly Ser Gly Glu  
515 520 525

Leu Gln Arg Gln Arg Val Met Glu Ala Val His Phe Arg Val Arg His  
530 535 540

Thr Ile Thr Ile Pro Asn Arg Gly Gly Pro Gly Gly Pro Asp Glu  
545 550 555 560

Trp Ala Asp Phe Gly Phe Asp Leu Pro Asp Cys Lys Ala Arg Lys Gln  
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Pro Ile Lys Glu Glu Phe Thr Glu Ala Glu Ile His  
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<210> 18

<211> 1817

<212> DNA

<213> Homo sapiens

<400> 18

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TCTCTGGAAC	CAGACAGCAC	CTACTTCGAC	CTTCCCCAGT	CAAGCCGGGG	GAATAATGAG	120
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GTGGTGGGCG	GAACGGATT	CAGCATGGAC	GTCTTCACC	TGGAGGGCAT	GACTACATCT	180
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GTCATGGCCC	AGTTCAATCT	GCTGAGCAGC	ACCATGGACC	AGATGAGCAG	CCGCGCGGCC	240
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TCGGCCAGCC	CCTACACCCC	AGAGCACGCC	GCCAGCGTGC	CCACCCACTC	GCCCTACGCA	300
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CAACCCAGCT	CCACCTTCGA	CACCATGTCG	CCGGCGCCTG	TCATCCCCTC	CAACACCGAC	360
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TACCCCGGAC	CCCACCACTT	TGAGGTCACT	TTCCAGCAGT	CCAGCACGGC	CAAGTCAGCC	420
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ACCTGGACGT	ACTCCCCGCT	CTTGAAGAAA	CTCTACTGCC	AGATCGCCAA	GACATGCC	480
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ATCCAGATCA	AGGTGTCCAC	CCCGCCACCC	CCAGGCCTG	CCATCCGGGC	CATGCCCTGTT	540
TACAAGAAAG	CGGAGCACGT	GACCGACGTC	GTGAAACGCT	GCCCCAACCA	CGAGCTCGGG	600
AGGGACTTCA	ACGAAGGACA	GTCTGCTCCA	GCCAGCCACC	TCATCCGCGT	GGAAGGCAAT	660
AATCTCTCGC	AGTATGTGGA	TGACCCCTGTC	ACCGGCAGGC	AGAGCGTCGT	GGTGCCCTAT	720
GAGCCACCAC	AGGTGGGGAC	GGAATTCAACC	ACCATCCTGT	ACAACTTCAT	GTGTAACAGC	780
AGCTGTGTAG	GGGGCATGAA	CCGGCGGCC	ATCCTCATCA	TCATCACCCCT	GGAGATGCGG	840
GATGGGCAGG	TGCTGGGCCG	CCGGTCCCTT	GAGGGCCGCA	TCTGCGCCTG	TCCTGGCCGC	900
GACCGAAAAG	CTGATGAGGA	CCACTACCGG	GAGCAGCAGG	CCCTGAACGA	GAGCTCCGCC	960
AAGAACGGGG	CCGCCAGCAA	GCGTGCCTTC	AAGCAGAGCC	CCCCTGCCGT	CCCCGCCCTT	1020
GGTGCCGGTG	TGAAGAACGCG	GCGGCATGGA	GACGAGGACA	CGTACTACCT	TCAGGTGCGA	1080
GGCCGGGAGA	ACTTGAGAT	CCTGATGAAG	CTGAAAGAGA	GCCTGGAGCT	GATGGAGTTG	1140
GTGCCGCAGC	CACTGGTGGA	CTCCTATCGG	CAGCAGCAGC	AGCTCCTACA	GAGGCCGAGT	1200
CACCTACAGC	CCCCGTCTA	CGGGCCGGTC	CTCTGCCCA	TGAACAAGGT	GCACGGGGC	1260
ATGAACAAGC	TGCCCTCCGT	CAACCAGCTG	GTGGGCCAGC	CTCCCCCGCA	CAGTTGGCA	1320
GCTACACCCA	ACCTGGGCC	CGTGGGCC	GGGATGCTCA	ACAACCATGG	CCACGCAGTG	1380
CCAGCCAACG	GCGAGATGAG	CAGCAGCCAC	AGCGCCAGT	CCATGGTCTC	GGGGTCCCAC	1440
TGCACTCCGC	CACCCCCCTA	CCACGCCGAC	CCCAGCCTCG	TCAGGACCTG	GGGGCCCTGA	1500
AGATCCCCGA	GCAGTACCGC	ATGACCATCT	GGCGGGCCT	GCAGGACCTG	AAGCAGGGCC	1560
ACGACTACAG	CACCGCGCAG	CAGCTGCTCC	GCTCTAGCAA	CGCGGCCACC	ATCTCCATCG	1620
GCGGCTCAGG	GGAACTGCAG	CGCCAGCGGG	TCATGGAGGC	CGTGCACTTC	CGCGTGCGCC	1680
ACACCATCAC	CATCCCCAAC	CGCGCGGCC	CAGGCAGCGG	CCCTGACGAG	TGGGCGGACT	1740
TCGGCTTCGA	CCTGCCGAC	TGCAAGGCC	GCAAGCAGCC	CATCAAGGAG	GAGTTCACGG	1800
AGGCCGAGAT	CCACTGA					1817

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 <213> Homo sapiens

<400> 19

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His Leu Trp Ser Ser Leu Glu Pro Asp Ser Thr Tyr Phe Asp Leu Pro  
 20 25 30

Gln Ser Ser Arg Gly Asn Asn Glu Val Val Gly Gly Thr Asp Ser Ser  
 35 40 45

Met Asp Val Phe His Leu Glu Gly Met Thr Thr Ser Val Met Ala Gln  
 50 55 60

Phe Asn Leu Leu Ser Ser Thr Met Asp Gln Met Ser Ser Arg Ala Ala  
 65 70 75 80

Ser Ala Ser Pro Tyr Thr Pro Glu His Ala Ala Ser Val Pro Thr His  
 85 90 95

Ser Pro Tyr Ala Gln Pro Ser Ser Thr Phe Asp Thr Met Ser Pro Ala  
 100 105 110

Pro Val Ile Pro Ser Asn Thr Asp Tyr Pro Gly Pro His His Phe Glu  
 115 120 125

Val Thr Phe Gln Gln Ser Ser Thr Ala Lys Ser Ala Thr Trp Thr Tyr  
 130 135 140

Ser Pro Leu Leu Lys Lys Leu Tyr Cys Gln Ile Ala Lys Thr Cys Pro  
 145 150 155 160

Ile Gln Ile Lys Val Ser Thr Pro Pro Pro Gly Thr Ala Ile Arg  
 165 170 175

Ala Met Pro Val Tyr Lys Lys Ala Glu His Val Thr Asp Val Val Lys  
 180 185 190

Arg Cys Pro Asn His Glu Leu Gly Arg Asp Phe Asn Glu Gly Gln Ser  
 195 200 205

Ala Pro Ala Ser His Leu Ile Arg Val Glu Gly Asn Asn Leu Ser Gln  
 210 215 220

Tyr Val Asp Asp Pro Val Thr Gly Arg Gln Ser Val Val Val Pro Tyr  
 225 230 235 240

Glu Pro Pro Gln Val Gly Thr Glu Phe Thr Thr Ile Leu Tyr Asn Phe  
 245 250 255

Met Cys Asn Ser Ser Cys Val Gly Gly Met Asn Arg Arg Pro Ile Leu  
 260 265 270

Ile Ile Ile Thr Leu Glu Met Arg Asp Gly Gln Val Leu Gly Arg Arg  
 275 280 285

Ser Phe Glu Gly Arg Ile Cys Ala Cys Pro Gly Arg Asp Arg Lys Ala  
 290 295 300

Asp Glu Asp His Tyr Arg Glu Gln Gln Ala Leu Asn Glu Ser Ser Ala  
 305 310 315 320

*ASJ*

Lys Asn Gly Ala Ala Ser Lys Arg Ala Phe Lys Gln Ser Pro Pro Ala  
 325 330 335

Val Pro Ala Leu Gly Ala Gly Val Lys Lys Arg Arg His Gly Asp Glu  
 340 345 350

Asp Thr Tyr Tyr Leu Gln Val Arg Gly Arg Glu Asn Phe Glu Ile Leu  
 355 360 365

Met Lys Leu Lys Glu Ser Leu Glu Leu Met Glu Leu Val Pro Gln Pro  
 370 375 380

Leu Val Asp Ser Tyr Arg Gln Gln Gln Gln Leu Leu Gln Arg Pro Ser  
 385 390 395 400

His Leu Gln Pro Pro Ser Tyr Gly Pro Val Leu Ser Pro Met Asn Lys  
 405 410 415

Val His Gly Gly Met Asn Lys Leu Pro Ser Val Asn Gln Leu Val Gly  
 420 425 430

Gln Pro Pro Pro His Ser Ser Ala Ala Thr Pro Asn Leu Gly Pro Val  
 435 440 445

Gly Pro Gly Met Leu Asn Asn His Gly His Ala Val Pro Ala Asn Gly  
 450 455 460

Glu Met Ser Ser Ser His Ser Ala Gln Ser Met Val Ser Gly Ser His  
 465 470 475 480

Cys Thr Pro Pro Pro Tyr His Ala Asp Pro Ser Leu Val Arg Thr  
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> 17  
> DNA  
> Artificial

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<211> 17  
<212> DNA  
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<220>  
<223> primer

<400> 20

GCGAGCTGCC CTCGGAG

<210> 21  
<211> 19  
<212> DNA  
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<220>  
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&lt;400&gt; 21

GGTTCTGCAG GTGACTCAG

19

<210> 22  
<211> 18  
<212> DNA  
<213> Artificial

<220>  
<223> primer

&lt;400&gt; 22

GCCATGCCTG TCTACAAG

18

<210> 23  
<211> 18  
<212> DNA  
<213> Artificial

<220>  
<223> antisense primer

&lt;400&gt; 23

ACCAGCTGGT TGACGGAG

18

*ASJ*  
<210> 24  
<211> 21  
<212> DNA  
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<220>  
<223> primer

&lt;400&gt; 24

GTCAAACCAGC TGGTGGGCCA G

21

<210> 25  
<211> 16  
<212> DNA  
<213> Artificial

<220>  
<223> antisense primer

&lt;400&gt; 25

GTGGATCTCG GCCTCC

16

&lt;210&gt; 26

<211> 17  
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 <213> Artificial  
  
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 <223> primer  
  
 <400> 26

AGGCCGGCGT GGGGAAG

17

<210> 27  
 <211> 19  
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 <400> 27

CTTGGCGATC TGGCAGTAG

19

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 <223> primer  
  
 <400> 28

*AS* GC GCCCACGA CCGTGAC

17

<210> 29  
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 <223> antisense primer  
  
 <400> 29

GGCAGCTTGG GTCTCTGG

18

<210> 30  
 <211> 18  
 <212> DNA  
 <213> Artificial  
  
 <220>  
 <223> primer

&lt;400&gt; 30

CTGTACGTCG GTGACCCCC

18

<210> 31  
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 <212> DNA  
 <213> Artificial  
  
 <220>  
 <223> antisense primer

<400> 31

TCAGTGGATC TCGGCCTC

18

<210> 32  
 <211> 18  
 <212> DNA  
 <213> Artificial

<220>  
 <223> primer

<400> 32

AGGGGACGCA GCGAAACC

18

<210> 33  
 <211> 19  
 <212> DNA  
 <213> Artificial

<220>  
 <223> antisense primer

<400> 33

CCATCAGCTC CAGGCTCTC

19

<210> 34  
 <211> 18  
 <212> DNA  
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<220>  
 <223> antisense primer

<400> 34

CCAGGACAGG CGCAGATG

18

<210> 35  
 <211> 19  
 <212> DNA  
 <213> Artificial

<220>  
 <223> antisense primer

<400> 35

GATGAGGTGG CTGGCTGGA

19

<210> 36

<211> 19

<212> DNA

<213> Artificial

<220>

<223> antisense primer

<400> 36

TGGTCAGGTT CTGCAGGTG

19

<210> 37

<211> 18

<212> DNA

<213> Artificial

<220>

<223> primer

<400> 37

CACCTACTCC AGGGATGC

18

<210> 38

<211> 21

<212> DNA

<213> Artificial

<220>

<223> antisense primer

<400> 38

*AS*  
AGGAAAATAG AAGCGTCAGT C

21

<210> 39

<211> 18

<212> DNA

<213> Artificial

<220>

<223> primer

<400> 39

CAGGCCCACT TGCCTGCC

18

<210> 40

<211> 19

<212> DNA

<213> Artificial

<220>

<223> antisense primer

&lt;400&gt; 40

CTGTCCCCAA GCTGATGAG

19

<210> 41  
<211> 15  
<212> DNA  
<213> Artificial

<220>  
<223> primer

<400> 41  
CCCCCCCCCC CCCCD

15

<210> 42  
<211> 16  
<212> DNA  
<213> Artificial

<220>  
<223> primer

<400> 42  
CCCCCCCCCC CCCCD

16

*ASJ*

<210> 43  
<211> 1400  
<212> DNA  
<213> Cebus apella

<400> 43

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gatcccagca tcgagcccc tctgagtcag gaaacattt cagacctatg gaaactactt 180
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 aggtgtgtgt cagaagcaaa 1400

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 <211> 393  
 <212> PRT  
 <213> Cebus apella

<400> 44  
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 Glu Thr Phe Ser Asp Leu Trp Lys Leu Leu Pro Glu Asn Asn Val Leu  
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 Ser Pro Leu Pro Ser Gln Ala Val Asp Asp Leu Met Leu Ser Pro Asp  
 35 40 45  
 Asp Leu Ala Gln Trp Leu Thr Glu Asp Pro Gly Pro Asp Glu Ala Pro  
 50 55 60  
 Arg Met Ser Glu Ala Ala Pro His Met Ala Pro Thr Pro Ala Ala Pro  
 65 70 75 80  
 Thr Pro Ala Ala Pro Ala Pro Ser Trp Pro Leu Ser Ser Ser  
 85 90 95  
 Val Pro Ser Gln Lys Thr Tyr His Gly Ser Tyr Gly Phe Arg Leu Gly  
 100 105 110  
 Phe Leu His Ser Gly Thr Ala Lys Ser Val Thr Cys Thr Tyr Ser Pro  
 115 120 125  
 Asp Leu Asn Lys Met Phe Cys Gln Leu Ala Lys Thr Cys Pro Val Gln  
 130 135 140  
 Leu Trp Val Asp Ser Thr Pro Pro Pro Gly Ser Arg Val Arg Ala Met  
 145 150 155 160  
 Ala Ile Tyr Lys Gln Ser Gln His Met Thr Glu Val Val Arg Arg Cys  
 165 170 175  
 Pro His His Glu Arg Cys Ser Asp Ser Asp Gly Leu Ala Pro Pro Gln  
 180 185 190  
 His Leu Ile Arg Val Glu Gly Asn Leu Arg Val Glu Tyr Ser Asp Asp  
 195 200 205  
 Arg Asn Thr Phe Arg His Ser Val Val Val Pro Tyr Glu Pro Pro Glu  
 210 215 220  
 Val Gly Ser Asp Cys Thr Thr Ile His Tyr Asn Tyr Met Cys Asn Ser  
 225 230 235 240  
 Ser Cys Met Gly Gly Met Asn Arg Arg Pro Ile Leu Thr Ile Ile Thr  
 245 250 255  
 Leu Glu Asp Ser Ser Gly Asn Leu Leu Gly Arg Asn Ser Phe Glu Val  
 260 265 270

Arg Val Cys Ala Cys Pro Gly Arg Asp Arg Arg Thr Glu Glu Glu Asn  
 275 280 285

Phe Arg Lys Lys Gly Glu Pro Cys His Glu Leu Pro Pro Gly Ser Thr  
 290 295 300

Lys Arg Ala Leu Pro Asn Asn Thr Ser Ser Ser Pro Gln Pro Lys Lys  
 305 310 315 320

Lys Pro Leu Asp Gly Glu Tyr Phe Thr Leu Gln Ile Arg Gly Arg Glu  
 325 330 335

Arg Phe Glu Met Phe Arg Glu Leu Asn Glu Ala Leu Glu Leu Lys Asp  
 340 345 350

Ala Gln Ala Gly Lys Glu Pro Ala Gly Ser Arg Ala His Ser Ser His  
 355 360 365

Leu Lys Ser Lys Lys Gly Gln Ser Thr Ser Arg His Lys Lys Phe Met  
 370 375 380

Phe Lys Thr Glu Gly Pro Asp Ser Asp  
 385 390

<210> 45  
<211> 393  
<212> PRT  
<213> Homo sapiens

*AS*  
<400> 45  
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Glu Thr Phe Ser Asp Leu Trp Lys Leu Leu Pro Glu Asn Asn Val Leu  
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Ser Pro Leu Pro Ser Gln Ala Met Asp Asp Leu Met Leu Ser Pro Asp  
 35 40 45

Asp Ile Glu Gln Trp Phe Thr Glu Asp Pro Gly Pro Asp Glu Ala Pro  
 50 55 60

Arg Met Pro Glu Ala Ala Pro Pro Val Ala Pro Ala Pro Ala Pro  
 65 70 75 80

Thr Pro Ala Ala Pro Ala Pro Ser Trp Pro Leu Ser Ser Ser  
 85 90 95

Val Pro Ser Gln Lys Thr Tyr Gln Gly Ser Tyr Gly Phe Arg Leu Gly  
 100 105 110

Phe Leu His Ser Gly Thr Ala Lys Ser Val Thr Cys Thr Tyr Ser Pro  
 115 120 125

Ala Leu Asn Lys Met Phe Cys Gln Leu Ala Lys Thr Cys Pro Val Gln  
 130 135 140

Leu Trp Val Asp Ser Thr Pro Pro Gly Thr Arg Val Arg Ala Met

46

145	150	155	160
Ala Ile Tyr Lys Gln Ser Gln His Met Thr Glu Val Val Arg Arg Cys			
165	170	175	
Pro His His Glu Arg Cys Ser Asp Ser Asp Gly Leu Ala Pro Pro Gln			
180	185	190	
His Leu Ile Arg Val Glu Gly Asn Leu Arg Val Glu Tyr Leu Asp Asp			
195	200	205	
Arg Asn Thr Phe Arg His Ser Val Val Val Pro Tyr Glu Pro Pro Glu			
210	215	220	
Val Gly Ser Asp Cys Thr Thr Ile His Tyr Asn Tyr Met Cys Asn Ser			
225	230	235	240
Ser Cys Met Gly Gly Met Asn Arg Arg Pro Ile Leu Thr Ile Ile Thr			
245	250	255	
Leu Glu Asp Ser Ser Gly Asn Leu Leu Gly Arg Asn Ser Phe Glu Val			
260	265	270	
Arg Val Cys Ala Cys Pro Gly Arg Asp Arg Arg Thr Glu Glu Glu Asn			
275	280	285	
Leu Arg Lys Lys Gly Glu Pro His His Glu Leu Pro Pro Gly Ser Thr			
290	295	300	
Lys Arg Ala Leu Pro Asn Asn Thr Ser Ser Pro Gln Pro Lys Lys			
305	310	315	320
Lys Pro Leu Asp Gly Glu Tyr Phe Thr Leu Gln Ile Arg Gly Arg Glu			
325	330	335	
Arg Phe Glu Met Phe Arg Glu Leu Asn Glu Ala Leu Glu Leu Lys Asp			
340	345	350	
Ala Gln Gln Gly Lys Glu Pro Gly Gly Arg Ser Ala His Ser Ser His			
355	360	365	
Leu Lys Ser Lys Lys Gly Gln Ser Thr Ser Arg His Lys Lys Leu Met			
370	375	380	
Phe Lys Thr Glu Gly Pro Asp Ser Asp			
385	390		

*ASW*

<210> 46  
<211> 889  
<212> DNA  
<213> Homo sapiens

<400> 46  
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gcgagctgcc ctcggaggcc ggctgtggga agatggccca gtccaccgcc acctcccc 180  
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tgctgcacta actggaccag agcaggagag gtggctccac actagtcttg ggctagcctt 480  
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 tgggaagggc aggagacgt a ggcctcacca ggagtctcag gctagccttg agctctggc 780  
 ctgggaggtt ttgggtgac acccaaactg gggactgacg ctcttatTTT cctctccctg 840  
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<210> 47  
 <211> 23  
 <212> DNA  
 <213> Artificial

<220>  
 <223> primer comprising BamHI site

<400> 47  
 gatccgggcc cttttttttt ttt

23

<210> 48  
 <211> 20  
 <212> DNA  
 <213> Artificial

<220>  
 <223> primer comprising ApaI site

<400> 48  
 aaaaaaaaaaa aaagggcccg

20

<210> 49  
 <211> 26  
 <212> DNA  
 <213> Artificial

<220>  
 <223> primer comprising Kpn I site

<400> 49  
 actggtaccg cgagctgccc tcggag

26

<210> 50  
 <211> 28  
 <212> DNA  
 <213> Artificial

<220>  
 <223> antisense primer comprising Xba I site

<400> 50  
 gactctagag gttctgcagg tgactcag

28

<210> 51  
 <211> 19  
 <212> DNA  
 <213> Artificial

<220>  
<223> primer

<400> 51  
gagcatgtga ccgacattg

19

<210> 52  
<211> 30  
<212> DNA  
<213> Artificial

<220>  
<223> primer comprising BamHI site

<400> 52  
tttggatccg tcaaccagct ggtgggccag

30

<210> 53  
<211> 25  
<212> DNA  
<213> Artificial

<220>  
<223> antisense primer comprising a Sal I site

<400> 53  
aaagtgcgacg tggatctcggt cctcc

25

*AS/*  
<210> 54  
<211> 27  
<212> DNA  
<213> Artificial

<220>  
<223> primer

<400> 54  
tatctcgagc tgtacgtcggt tgacccc

27

<210> 55  
<211> 27  
<212> DNA  
<213> Artificial

<220>  
<223> antisense primer

<400> 55  
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27